

1647RUSH

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Form 07
20

CRF Errors Corrected by the STIC System Branch

Serial Number: 09/263,022

ENTERED

CRF Processing Date: 5/7/2001
Edited by: AZ
Verified by: AZ (STIC staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: 16,26

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/263,022

DATE: 05/07/2001
TIME: 13:18:48

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05072001\I263022.raw

PS

2 <110> APPLICANT: McCarthy, Sean A.
4 <120> TITLE OF INVENTION: NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
5 MOLECULES AND USES THEREFOR
7 <130> FILE REFERENCE: MNI-108CP2
9 <140> CURRENT APPLICATION NUMBER: 09/263,022
10 <141> CURRENT FILING DATE: 1999-03-05
12 <150> PRIOR APPLICATION NUMBER: 08/843,704
13 <151> PRIOR FILING DATE: 1997-04-16
15 <150> PRIOR APPLICATION NUMBER: 08/842,898
16 <151> PRIOR FILING DATE: 1997-04-17
18 <150> PRIOR APPLICATION NUMBER: 60/071,589
19 <151> PRIOR FILING DATE: 1998-01-15
21 <150> PRIOR APPLICATION NUMBER: 09/009,802
22 <151> PRIOR FILING DATE: 1998-01-20
24 <160> NUMBER OF SEQ ID NOS: 38
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2479
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (38)..(1087)
37 <220> FEATURE:
38 <223> OTHER INFORMATION: 'n' at position 1146 may be any nucleotide
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41 ggcacgaggg ggcggcggtc gccccggcag agcggag atg cag cgg ctt ggg gcc 55
42 Met Gln Arg Leu Gly Ala
43 1 5
45 acc ctg ctg tgc ctg ctg gcg gcg gtc ccc acg gcc ccc gcg 103
46 Thr Leu Leu Cys Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
47 10 15 20
49 ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
50 Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
51 25 30 35
53 agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc ccg gag gtt 199
54 Ser Tyr Pro Gln Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
55 40 45 50
57 gag gaa ctg atg gag gac acg cag cac aaa ttg ccg agc gcg gtg gaa 247
58 Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
59 55 60 65 70
61 gag atg gag gca gaa gaa gct gct aaa gca tca tca gaa gtg aac 295
62 Glu Met Glu Ala Glu Ala Ala Lys Ala Ser Ser Glu Val Asn
63 75 80 85
65 ctg gca aac tta cct ccc acg tat cac aat gag acc aac aca gac acg 343
66 Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr
67 90 95 100

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/263,022

DATE: 05/07/2001
TIME: 13:18:48

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05072001\I263022.raw

69 aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata	391
70 Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
71 105 110 115	
73 acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca	439
74 Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
75 120 125 130	
77 tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac	487
78 Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
79 135 140 145 150	
81 gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac	535
82 Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	
83 155 160 165	
85 acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt	583
86 Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
87 170 175 180	
89 gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg	631
90 Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
91 185 190 195	
93 gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc	679
94 Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
95 200 205 210	
97 cag ccc ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg	727
98 Gln Pro Gly Leu Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
99 215 220 225 230	
101 tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc	775
102 Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
103 235 240 245	
105 cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg	823
106 Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
107 250 255 260	
109 gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac	871
110 Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
111 265 270 275	
113 agc ctg gtg tat gtg tgc aag ccc acc ttc gtg ggg agc cgt gac caa	919
114 Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
115 280 285 290	
117 gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt	967
118 Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val	
119 295 300 305 310	
121 ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg	1015
122 Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg	
123 315 320 325	
125 agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct	1063
126 Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala	
127 330 335 340	
129 gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggttagatgtg	1117
130 Ala Leu Leu Gly Arg Glu Glu Ile	
131 345 350	
133 caatagaaat agctaattta tttcccccang ttgtgtgcttt aagcgtggc tgaccaggct	1177

WOF

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/263,022DATE: 05/07/2001
TIME: 13:18:48Input Set : A:\Pto.amc
Output Set: N:\CRF3\05072001\I263022.raw

135 tcttcctaca tcttcttccc agtaagttc ccctctggct tgacagcatg aggtgttgc 1237
 137 catttggca gctcccccag gctgttctcc aggcttcaca gtctggct tggagagtc 1297
 139 agcagggtt aaactgcagg agcagttgc caccctgtc cagattattg gctgcttgc 1357
 141 ctctaccagt tggcagacag ccgttgcattc tacatggctt tgataattgt ttgagggag 1417
 143 gagatggaaa caatgtggag tctccctctg attggtttg gggaaatgtg gagaagagtg 1477
 145 ccctgcttgc caaacatcaa cctggcaaaa atgcaacaaa tgaatttcc acgcagttct 1537
 147 ttccatgggc ataggtaaac tgcgttgcattc gctgttgcag atgaaatgtt ctgttccaccc 1597
 149 tgcattacat gtgttattt atccagcagt gttgctcagc tcctacccgt gtgccaggc 1657
 151 agcattttca tatccaagat caattccctc tctcagcaca gcctggggag gggtcattg 1717
 153 ttctcctcgatccatcaggat tttcagggc ttagagactg caagctgttcc gccaagtca 1777
 155 cacagctagt gaagaccaga gcagttcat ctgggtgtga ctctaaatctc agtgcctct 1837
 157 ccactacccc acaccagcct tggtgccacc aaaagtgcct cccaaaagga aggagaatgg 1897
 159 gattttctt ttgaggcatg cacatcttggaa attaaggta aactaattctt cccatccctc 1957
 161 taaaagtaaa ctactgttag gaacagcagt gttctcacag tggggcag ccgtccttct 2017
 163 aatgaagaca atgatatttgc cactgtccctt ctttggcagt tgcatttaga actttgaaag 2077
 165 gtatatgact gagcgttagca tacaggttac cctgcagaaa cagtagtttgc gtaattgttag 2137
 167 ggcgaggatt ataaatgaaa ttgcacaaat cacttagcag caactgaaagaa caattatcaa 2197
 169 ccacgtggag aaaatcaaaac cgagcaggc tgggtgaaac atgggtgttac tatgcactg 2257
 171 cgaacactga actctacgcc actccacaaa tgatgttttc aggtgttgc gactgttgc 2317
 173 accatgttcatccatcaggat tcttaaaggat taaagttgcat catgattgtttaaagcatgt 2377
 175 ttctttgtgtttaaattt gtataaacat aagttgcatt tagaaatcaa gcataaatca 2437
 177 cttcaactgc taaaaaaaaaaaaaaaaaaaaaaa aa 2479

180 <210> SEQ ID NO: 2
 181 <211> LENGTH: 350
 182 <212> TYPE: PRT
 183 <213> ORGANISM: Homo sapiens
 185 <400> SEQUENCE: 2

186 Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
 187 1 5 10 15
 188 Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
 189 20 25 30
 190 Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 191 35 40 45
 192 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 193 50 55 60
 194 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 195 65 70 75 80
 196 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 197 85 90 95
 198 Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
 199 100 105 110
 200 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 201 115 120 125
 202 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 203 130 135 140
 204 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 205 145 150 155 160
 206 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 207 165 170 175

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/263,022

DATE: 05/07/2001

TIME: 13:18:48

Input Set : A:\Pto.amc

Output Set: N:\CRF3\05072001\I263022.raw

219 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 220 180 185 190
 222 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 223 195 200 205
 225 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 226 210 215 220
 228 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 229 225 230 235 240
 231 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 232 245 250 255
 234 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 235 260 265 270
 237 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 238 275 280 285
 240 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 241 290 295 300
 243 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 244 305 310 315 320
 246 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
 247 325 330 335
 249 Pro Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
 250 340 345 350
 253 <210> SEQ ID NO: 3
 254 <211> LENGTH: 1050
 255 <212> TYPE: DNA
 256 <213> ORGANISM: Homo sapiens
 258 <220> FEATURE:
 259 <221> NAME/KEY: CDS
 260 <222> LOCATION: (1)..(1050)
 262 <400> SEQUENCE: 3
 263 atg cag cgg ctt ggg gcc acc ctg ctg tgc ctg ctg ctg gcg gcg gcg 48
 264 Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
 265 1 5 10 15
 267 gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc 96
 268 Val Pro Thr Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
 269 20 25 30
 271 aag ccc ggc ccg gct ctc agc tac ccg cag gag gag gcc acc ctc aat 144
 272 Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 273 35 40 45
 275 gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa 192
 276 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 277 50 55 60
 279 ttg cgc agc gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa 240
 280 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 281 65 70 75 80
 283 gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat 288
 284 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 285 85 90 95
 287 gag acc aac aca gac aac gtt gga aat aat acc atc cat gtg cac 336

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/263,022

DATE: 05/07/2001
TIME: 13:18:49

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05072001\I263022.raw

288 Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
289 100 105 110
291 cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt 384
292 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
293 115 120 125
295 tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc 432
296 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
297 130 135 140
299 cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag 480
300 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
301 145 150 155 160
303 ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg 528
304 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
305 165 170 175
307 ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg 576
308 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
309 180 185 190
311 ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt 624
312 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
313 195 200 205
315 gac aac cag agg gac tgc cag ccc ggg ctg tgc tgt gcc ttc cag aga 672
316 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
317 210 215 220
319 ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt 720
320 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
321 225 230 235 240
323 tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta 768
324 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
325 245 250 255
327 gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc 816
328 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
329 260 265 270
331 tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccc acc ttc 864
332 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
333 275 280 285
335 gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc 912
336 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
337 290 295 300
339 ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag 960
340 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
341 305 310 315 320
343 ctg gag gac ctg gag agg agc ctg act gaa gag atg ggc ctg agg gag 1008
344 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
345 325 330 335
347 cct gcg gct gcc gct gca ctg ctg gga agg gaa gag att 1050
348 Pro Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
349 340 345 350
352 <210> SEQ ID NO: 4
353 <211> LENGTH: 848

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/263,022DATE: 05/07/2001
TIME: 13:18:50Input Set : A:\Pto.amc
Output Set: N:\CRF3\05072001\I263022.raw

L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1820 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1820 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1823 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1823 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1826 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1826 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1829 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1829 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1853 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1853 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1856 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1856 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1859 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1859 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1862 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1862 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1865 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1865 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1868 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1868 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1871 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1871 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
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L:1874 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1874 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1874 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
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L:2118 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
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L:2121 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2124 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
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L:2127 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/263,022

DATE: 05/07/2001
TIME: 13:18:50

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05072001\I263022.raw

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L:2188 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:2188 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:2188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/263,022

DATE: 05/07/2001
TIME: 13:01:40

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05072001\I263022.raw

Does Not Comply
Corrected Diskette Needed

6 <110> APPLICANT: McCarthy, Sean A.
8 <120> TITLE OF INVENTION: NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
9 MOLECULES AND USES THEREFOR
11 <130> FILE REFERENCE: MNI-108CP2
13 <140> CURRENT APPLICATION NUMBER: 09/263,022
C--> 14 <141> CURRENT FILING DATE: 2000-02-26
16 <150> PRIOR APPLICATION NUMBER: 08/843,704
17 <151> PRIOR FILING DATE: 1997-04-16
19 <150> PRIOR APPLICATION NUMBER: 08/842,898
20 <151> PRIOR FILING DATE: 1997-04-17
22 <150> PRIOR APPLICATION NUMBER: 60/071,589
23 <151> PRIOR FILING DATE: 1998-01-15
25 <150> PRIOR APPLICATION NUMBER: 09/009,802
26 <151> PRIOR FILING DATE: 1998-01-20
28 <160> NUMBER OF SEQ ID NOS: 38
30 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

1163 <210> SEQ ID NO: 16
1164 <211> LENGTH: 2380
1165 <212> TYPE: DNA
1166 <213> ORGANISM: Homo sapiens
1168 <220> FEATURE:
1169 <221> NAME/KEY: CDS
1170 <222> LOCATION: (109)..(1155)
E--> 1172 <400> SEQUENCE: 26/16
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1175 gtcagcttt gttcattcga attgggcggc ggccagcgcg gaacaaac atg cag cgg 117
1176 Met Gln Arg
1177 1
1179 ctc ggg ggt att ttg ctg tgc aca ctg ctg gcg gcg gtc ccc act 165
1180 Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr
1181 5 10 15
1183 gct cct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc 213
1184 Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly
1185 20 25 30 35
1187 cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt 261
1188 Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe
1189 40 45 50
1191 cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt 309
1192 Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser
1193 55 60 65
1195 gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct 357
1196 Ala Val Glu Glu Met Glu Ala Glu Ala Ala Lys Thr Ser Ser
1197 70 75 80

RAW SEQUENCE LISTING

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DATE: 05/07/2001

TIME: 13:01:40

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\05072001\I263022.raw

1199 gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc	405
1200 Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser	
1201 85 90 95	
1203 acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt	453
1204 Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val	
1205 100 105 110 115	
1207 cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca	501
1208 His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr	
1209 120 125 130	
1211 gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt	549
1212 Val Ile Thr Ser Val Gly Asp Glu Glu Lys Arg Ser His Glu Cys	
1213 135 140 145	
1215 atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc	597
1216 Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser	
1217 150 155 160	
1219 ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc	645
1220 Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr	
1221 165 170 175	
1223 cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc	693
1224 Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys	
1225 180 185 190 195	
1227 acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag	741
1228 Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln	
1229 200 205 210	
1231 agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg	789
1232 Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu	
1233 215 220 225	
1235 ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac	837
1236 Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp	
1237 230 235 240	
1239 ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa	885
1240 Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu	
1241 245 250 255	
1243 gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca	933
1244 Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro	
1245 260 265 270 275	
1247 cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc	981
1248 His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser	
1249 280 285 290	
1251 cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag	1029
1252 His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu	
1253 295 300 305	
1255 tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac	1077
1256 Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp	
1257 310 315 320	
1259 ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct	1125
1260 Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro	
1261 325 330 335	
1263 gtg gag tca cta ggc gga gag gag att taggccccaga cccagctgag	1175

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Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\05072001\I263022.raw

1264 Val Glu Ser Leu Gly Gly Glu Glu Ile
 1265 340 345
 1267 tcactggtag atgtgcata gaaatggcta atttatttc ccaggagtgt ccccaagtgt 1235
 1269 ggaatggccg cagctccctc ccagtagctt ttccctctggc ttgacaaggt acagtgcagt 1295
 1271 acatttcttc cagccgcctc gcttctctga cttggaaag acaggcatgg cggtaaggg 1355
 1273 cageggtag tcgtccctcg ctgttgc tag aaacgctgtc ttgttctca tggatggaa 1415
 1275 atttgcgttga agggagagga tggaaagggg tgaagtctgc tcatgatgga tttggggat 1475
 1277 acagggagga ggatgcctgc ctgcagac tggacttgc aaaaatgtaac ctttgctttt 1535
 1279 gtcttgcgc gctccatgg gctgaggcag tggctacaca agagctatgc tgctctgtgg 1595
 1281 cctccacat attcatccct gtgttgcgc tcctacctca ctgtcagcac agcccttcat 1655
 1283 agccacgccc cctctgtctc accacagcct aggagggac cagagggac ttctctcaga 1715
 1285 gcccattgtc ctctctctca accccatacc agcctctgtc ccagcagac tccctccaaa 1775
 1287 tggaggaggt gaaatccctt ggttaatta ttttctcctt caaggcacgc ctgcccactaa 1835
 1289 ggtcaggctg acttgatgt ccctctaacc ttctgtgcag tgggtggac actgtcttcc 1895
 1291 accgactgtc tcaatacctc taaaagccag tgctcgagg gcagtcgtg taaattaatt 1955
 1293 tgcaggaaat atacttggct aattgttaggg ctaggattgt gaatgaaatt tgcaaagtgc 2015
 1295 ctttagcaaca atggaaagcc ttttcagtc acaccggaaa gtcacaacca agccagggtt 2075
 1297 ttagaggtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggcctcaga 2135
 1299 tgacggtttcc aggtgccagg aactattacc attctgttac tatccagagt tattaaaatt 2195
 1301 gaaatgtca cacattgtta taagcatgcc tttctctga gttttaatt atatgtatac 2255
 1303 aaaaacatgt ggcctcaaa gatcatgcac aaaccactac tctttgtcaa ttcttgact 2315
 1305 tttctctttt atttcaata aatacaaatac cccttcatgc aaaaaaaaaaaa aaaaaggcgc 2375
 1307 gcccgc 2380

1907 <210> SEQ ID NO: 26

1908 <211> LENGTH: 835

1909 <212> TYPE: DNA

1910 <213> ORGANISM: Mus musculus

1912 <220> FEATURE:

1913 <221> NAME/KEY: CDS

1914 <222> LOCATION: (57)..(746)

E--> 1916 <400> SEQUENCE: (25) 26

1917 gaattcggca cgaggcagaa ggcgcgaatg aaggcaaagc ctcccaccca cctgca atg 59
 1918 Met
 1919 1
 1920 tgcgttgc 107
 1921 tgt cga ctg agg gtc ttg ctg ctg ctg ctc ccc ttg gcc ttc gtg tcc 107
 1922 Cys Arg Leu Arg Val Leu Leu Leu Leu Pro Leu Ala Phe Val Ser
 1923 5 10 15
 1924 tcc tct gct ctc ccc atc cat gat gtc gac tct cag cag aac acc tcc 155
 1925 Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr Ser
 1926 20 25 30
 1927 ggg ttc ctg ggc ctt cag agg ctt ctc caa agc ttt agt cga ctg ttc 203
 1928 Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu Phe
 1929 35 40 45
 1930 45
 1931 50 55 60 65
 1932 65
 1933 70 75 80
 1934 80
 1935 85
 1936 90
 1937 95
 1938 100
 1939 105

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Input Set : A:\Seqlist.txt
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1941	gag	cac	aga	atg	ggc	aac	cat	acc	ctc	tcc	agc	cac	cta	cag	ata	gac	347	
1942	Glu	His	Arg	Met	Gly	Asn	His	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp		
1943				85					90					95				
1945	aag	gtg	act	gac	aac	cag	aca	ggg	gag	gtg	cac	atc	tcg	gag	aaa	gtc	395	
1946	Lys	Val	Thr	Asp	Asn	Gln	Thr	Gly	Glu	Val	His	Ile	Ser	Glu	Lys	Val		
1947				100				105			105		110					
1949	gag	gcc	tcc	att	gag	cca	gaa	cg	aac	ccg	gaa	ggg	gac	tgg	aag	gtt	443	
1950	Glu	Ala	Ser	Ile	Glu	Pro	Glu	Arg	Asn	Pro	Glu	Gly	Asp	Trp	Lys	Val		
1951		115				120				125								
1953	ccc	aaa	gta	gaa	gca	aaa	gag	ccc	ccg	gtg	cct	gtg	cag	aag	gtc	acc	491	
1954	Pro	Lys	Val	Glu	Ala	Lys	Glu	Pro	Pro	Val	Pro	Val	Gln	Lys	Val	Thr		
1955	130				135				140			140		145				
1957	gac	agc	ttg	cac	cca	gag	ccc	cg	cag	gtg	gct	ttc	tgg	atc	atg	aag	539	
1958	Asp	Ser	Leu	His	Pro	Glu	Pro	Arg	Gln	Val	Ala	Phe	Trp	Ile	Met	Lys		
1959				150				155			155		160					
1961	atg	cca	agg	cg	agg	acc	cag	ccc	gat	gtc	cag	gat	gga	ggc	cg	tgg	587	
1962	Met	Pro	Arg	Arg	Arg	Thr	Gln	Pro	Asp	Val	Gln	Asp	Gly	Gly	Arg	Trp		
1963		165				170			175									
1965	ctc	ata	gaa	aag	cga	cat	cg	atg	cag	gcc	atc	cg	gat	ggg	ctc	cgt	635	
1966	Leu	Ile	Glu	Lys	Arg	His	Arg	Met	Gln	Ala	Ile	Arg	Asp	Gly	Leu	Arg		
1967		180			185			190										
1969	gga	ggc	gcc	cgt	gag	gac	agc	ctg	gag	gat	ggg	gtc	cat	atc	ccc	caa	683	
1970	Gly	Gly	Ala	Arg	Glu	Asp	Ser	Leu	Glu	Asp	Gly	Val	His	Ile	Pro	Gln		
1971		195			200			205										
1973	cac	gcc	aag	ctg	cct	gtc	aga	aag	aca	cac	ttt	ctc	tac	atc	ctc	agg	731	
1974	His	Ala	Lys	Leu	Pro	Val	Arg	Lys	Thr	His	Phe	Leu	Tyr	Ile	Leu	Arg		
1975	210		215			220			225									
1977	cca	tcc	caa	cag	ctg	taagtggg	ga	ccagatgtcc	cacacc	ctac	ccca	acacca					786	
1978	Pro	Ser	Gln	Gln	Leu													
1979			230															
1981	tatggaaata	aagg	ttt	tct	tacat	ctaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaa	835								

VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\05072001\I263022.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1172 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:26
L:1824 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1824 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1827 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1827 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1830 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1830 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1833 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1833 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1857 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1857 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1860 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1860 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1860 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1863 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1863 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1866 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1866 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1866 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1869 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1869 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1872 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1872 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1875 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1875 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1878 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1878 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1916 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:25
L:2122 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:2122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2125 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:2125 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:2125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2128 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:2128 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29

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Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05072001\I263022.raw

L:2128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2131 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:2131 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:2131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2192 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:2192 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:2192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34